

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/594,690
Source: IFWP
Date Processed by STIC: 10/6/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 10/06/2006

PATENT APPLICATION: US/10/594,690

TIME: 10:49:29

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\10062006\J594690.raw

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3 <110> APPLICANT: Kodama, Tatsuhiko
4     Yamada, Yoshiki
5     Kamada, Nobuo
6     Jishage, Kou-ichi
10 <120> TITLE OF INVENTION: Nonhuman animals for antibody production, and methods and
systems for
11     producing antibodies using such animals
13 <130> FILE REFERENCE: 14875-167US1
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/594,690
C--> 15 <141> CURRENT FILING DATE: 2006-09-28
15 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/006298
16 <151> PRIOR FILING DATE: 2005-03-31
18 <150> PRIOR APPLICATION NUMBER: JP2004-107669
19 <151> PRIOR FILING DATE: 2004-03-31
21 <160> NUMBER OF SEQ ID NOS: 10
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1539
27 <212> TYPE: DNA
28 <213> ORGANISM: Baculovirus
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1539)
35 <400> SEQUENCE: 1
36 atg gta agc gct att gtt tta tat gtg ctt ttg gcg gcg gcg gcg cat      48
37 Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala Ala His
38 1          5          10          15
40 tct gcc ttt gcg gcg gag cac tgc aac gcg caa atg aag acg ggt ccg      96
41 Ser Ala Phe Ala Ala Glu His Cys Asn Ala Gln Met Lys Thr Gly Pro
42          20          25          30
44 tac aag att aaa aac ttg gac att acc ccg ccc aag gaa acg ctg caa      144
45 Tyr Lys Ile Lys Asn Leu Asp Ile Thr Pro Pro Lys Glu Thr Leu Gln
46          35          40          45
48 aag gac gtg gaa atc acc atc gtg gag acg gac tac aac gaa aac gtg      192
49 Lys Asp Val Glu Ile Thr Ile Val Glu Thr Asp Tyr Asn Glu Asn Val
50          50          55          60
52 att atc ggc tac aag ggg tac tac cag gcg tat gcg tac aac ggc ggc      240
53 Ile Ile Gly Tyr Lys Gly Tyr Tyr Gln Ala Tyr Ala Tyr Asn Gly Gly
54 65          70          75          80
56 tcg ctg gat ccc aac aca cgc gtc gaa gaa acc atg aaa acg ctg aat      288
57 Ser Leu Asp Pro Asn Thr Arg Val Glu Glu Thr Met Lys Thr Leu Asn
58          85          90          95
60 gtg ggc aaa gag gat ttg ctt atg tgg agc atc agg cag cag tgc gag      336
61 Val Gly Lys Glu Asp Leu Leu Met Trp Ser Ile Arg Gln Gln Cys Glu

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62	100	105	110	
64	gtg ggc gaa gag ctg atc gac cgt tgg ggc agt gac agc gac gac tgt	384		
65	Val Gly Glu Glu Leu Ile Asp Arg Trp Gly Ser Asp Ser Asp Asp Cys			
66	115 120 125			
68	ttt cgc gac aac gag ggc cgc ggc cag tgg gtc aaa ggc aaa gag ttg	432		
69	Phe Arg Asp Asn Glu Gly Arg Gly Gln Trp Val Lys Gly Lys Glu Leu			
70	130 135 140			
72	gtg aag cgg cag aat aac aat cac ttt gcg cac cac acg tgc aac aaa	480		
73	Val Lys Arg Gln Asn Asn Asn His Phe Ala His His Thr Cys Asn Lys			
74	145 150 155 160			
76	tcg tgg cga tgc ggc att tcc act tcg aaa atg tac agc agg ctc gag	528		
77	Ser Trp Arg Cys Gly Ile Ser Thr Ser Lys Met Tyr Ser Arg Leu Glu			
78	165 170 175			
80	tgc cag gac gac acg gac gag tgc cag gta tac att ttg gac gct gag	576		
81	Cys Gln Asp Asp Thr Asp Glu Cys Gln Val Tyr Ile Leu Asp Ala Glu			
82	180 185 190			
84	ggc aac ccc atc aac gtg acc gtg gac act gtg ctt cat cga gac ggc	624		
85	Gly Asn Pro Ile Asn Val Thr Val Asp Thr Val Leu His Arg Asp Gly			
86	195 200 205			
88	gtg agt atg att ctc aaa caa aag tct acg ttc acc acg cgc caa ata	672		
89	Val Ser Met Ile Leu Lys Gln Lys Ser Thr Phe Thr Thr Arg Gln Ile			
90	210 215 220			
92	aaa gct gcg tgt ctg ctc att aaa gat gac aaa aat aac ccc gag tcg	720		
93	Lys Ala Ala Cys Leu Leu Ile Lys Asp Asp Lys Asn Asn Pro Glu Ser			
94	225 230 235 240			
96	gtg aca cgc gaa cac tgt ttg att gac aat gat ata tat gat ctt tct	768		
97	Val Thr Arg Glu His Cys Leu Ile Asp Asn Asp Ile Tyr Asp Leu Ser			
98	245 250 255			
100	aaa aac acg tgg aac tgc aag ttt aac aga tgc att aaa cgc aaa gtc	816		
101	Lys Asn Thr Trp Asn Cys Lys Phe Asn Arg Cys Ile Lys Arg Lys Val			
102	260 265 270			
104	gag cac cga gtc aag aag cgg ccg ccc act tgg cgc cac aac gtt aga	864		
105	Glu His Arg Val Lys Lys Arg Pro Pro Thr Trp Arg His Asn Val Arg			
106	275 280 285			
108	gcc aag tac aca gag gga gac act gcc acc aaa ggc gac ctg atg cat	912		
109	Ala Lys Tyr Thr Glu Gly Asp Thr Ala Thr Lys Gly Asp Leu Met His			
110	290 295 300			
112	att caa gag gag ctg atg tac gaa aac gat ttg ctg aaa atg aac att	960		
113	Ile Gln Glu Glu Leu Met Tyr Glu Asn Asp Leu Leu Lys Met Asn Ile			
114	305 310 315 320			
116	gag ctg atg cat gcg cac atc aac aag cta aac aat atg ctg cac gac	1008		
117	Glu Leu Met His Ala His Ile Asn Lys Leu Asn Asn Met Leu His Asp			
118	325 330 335			
120	ctg ata gtc tcc gtg gcc aag gtg gac gag cgt ttg att ggc aat ctc	1056		
121	Leu Ile Val Ser Val Ala Lys Val Asp Glu Arg Leu Ile Gly Asn Leu			
122	340 345 350			
124	atg aac aac tct gtt tct tca aca ttt ttg tcg gac gac acg ttt ttg	1104		
125	Met Asn Asn Ser Val Ser Ser Thr Phe Leu Ser Asp Asp Thr Phe Leu			
126	355 360 365			

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128 ctg atg ccg tgc acc aat ccg ccg gca cac acc agt aat tgc tac aac      1152
129 Leu Met Pro Cys Thr Asn Pro Pro Ala His Thr Ser Asn Cys Tyr Asn
130      370      375      380
132 aac agc atc tac aaa gaa ggg cgt tgg gtg gcc aac acg gac tgc tgc      1200
133 Asn Ser Ile Tyr Lys Glu Gly Arg Trp Val Ala Asn Thr Asp Ser Ser
134 385      390      395      400
136 caa tgc ata gat ttt agc aac tac aag gaa cta gca att gac gac gac      1248
137 Gln Cys Ile Asp Phe Ser Asn Tyr Lys Glu Leu Ala Ile Asp Asp Asp
138      405      410      415
140 gtc gag ttt tgg atc ccg acc atc ggc aac acg acc tat cac gac agt      1296
141 Val Glu Phe Trp Ile Pro Thr Ile Gly Asn Thr Thr Tyr His Asp Ser
142      420      425      430
144 tgg aaa gat gcc agc ggc tgg tgc ttt att gcc caa caa aaa agc aac      1344
145 Trp Lys Asp Ala Ser Gly Trp Ser Phe Ile Ala Gln Gln Lys Ser Asn
146      435      440      445
148 ctc ata acc acc atg gag aac acc aag ttt ggc ggc gtc ggc acc agt      1392
149 Leu Ile Thr Thr Met Glu Asn Thr Lys Phe Gly Gly Val Gly Thr Ser
150      450      455      460
152 ctg agc gac atc act tcc atg gct gaa ggc gaa ttg gcc gct aaa ttg      1440
153 Leu Ser Asp Ile Thr Ser Met Ala Glu Gly Glu Leu Ala Ala Lys Leu
154 465      470      475      480
156 act tgc ttc atg ttt ggt cat gta gtt aac ttt gta att ata tta att      1488
157 Thr Ser Phe Met Phe Gly His Val Val Asn Phe Val Ile Ile Leu Ile
158      485      490      495
160 gtg att tta ttt ttg tac tgt atg att aga aac cgt aat aga caa tat      1536
161 Val Ile Leu Phe Leu Tyr Cys Met Ile Arg Asn Arg Asn Arg Gln Tyr
162      500      505      510
164 taa      1539
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 512
169 <212> TYPE: PRT
170 <213> ORGANISM: Baculovirus
172 <400> SEQUENCE: 2
173 Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala Ala His
174 1      5      10      15
176 Ser Ala Phe Ala Ala Glu His Cys Asn Ala Gln Met Lys Thr Gly Pro
177      20      25      30
179 Tyr Lys Ile Lys Asn Leu Asp Ile Thr Pro Pro Lys Glu Thr Leu Gln
180      35      40      45
182 Lys Asp Val Glu Ile Thr Ile Val Glu Thr Asp Tyr Asn Glu Asn Val
183      50      55      60
185 Ile Ile Gly Tyr Lys Gly Tyr Tyr Gln Ala Tyr Ala Tyr Asn Gly Gly
186 65      70      75      80
188 Ser Leu Asp Pro Asn Thr Arg Val Glu Glu Thr Met Lys Thr Leu Asn
189      85      90      95
191 Val Gly Lys Glu Asp Leu Leu Met Trp Ser Ile Arg Gln Gln Cys Glu
192      100      105      110
194 Val Gly Glu Glu Leu Ile Asp Arg Trp Gly Ser Asp Ser Asp Asp Cys
195      115      120      125

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197 Phe Arg Asp Asn Glu Gly Arg Gly Gln Trp Val Lys Gly Lys Glu Leu
198      130      135      140
200 Val Lys Arg Gln Asn Asn Asn His Phe Ala His His Thr Cys Asn Lys
201 145      150      155      160
203 Ser Trp Arg Cys Gly Ile Ser Thr Ser Lys Met Tyr Ser Arg Leu Glu
204      165      170      175
206 Cys Gln Asp Asp Thr Asp Glu Cys Gln Val Tyr Ile Leu Asp Ala Glu
207      180      185      190
209 Gly Asn Pro Ile Asn Val Thr Val Asp Thr Val Leu His Arg Asp Gly
210      195      200      205
212 Val Ser Met Ile Leu Lys Gln Lys Ser Thr Phe Thr Thr Arg Gln Ile
213      210      215      220
215 Lys Ala Ala Cys Leu Leu Ile Lys Asp Asp Lys Asn Asn Pro Glu Ser
216 225      230      235      240
218 Val Thr Arg Glu His Cys Leu Ile Asp Asn Asp Ile Tyr Asp Leu Ser
219      245      250      255
221 Lys Asn Thr Trp Asn Cys Lys Phe Asn Arg Cys Ile Lys Arg Lys Val
222      260      265      270
224 Glu His Arg Val Lys Lys Arg Pro Pro Thr Trp Arg His Asn Val Arg
225      275      280      285
227 Ala Lys Tyr Thr Glu Gly Asp Thr Ala Thr Lys Gly Asp Leu Met His
228      290      295      300
230 Ile Gln Glu Glu Leu Met Tyr Glu Asn Asp Leu Leu Lys Met Asn Ile
231 305      310      315      320
233 Glu Leu Met His Ala His Ile Asn Lys Leu Asn Asn Met Leu His Asp
234      325      330      335
236 Leu Ile Val Ser Val Ala Lys Val Asp Glu Arg Leu Ile Gly Asn Leu
237      340      345      350
239 Met Asn Asn Ser Val Ser Ser Thr Phe Leu Ser Asp Asp Thr Phe Leu
240      355      360      365
242 Leu Met Pro Cys Thr Asn Pro Pro Ala His Thr Ser Asn Cys Tyr Asn
243      370      375      380
245 Asn Ser Ile Tyr Lys Glu Gly Arg Trp Val Ala Asn Thr Asp Ser Ser
246 385      390      395      400
248 Gln Cys Ile Asp Phe Ser Asn Tyr Lys Glu Leu Ala Ile Asp Asp Asp
249      405      410      415
251 Val Glu Phe Trp Ile Pro Thr Ile Gly Asn Thr Thr Tyr His Asp Ser
252      420      425      430
254 Trp Lys Asp Ala Ser Gly Trp Ser Phe Ile Ala Gln Gln Lys Ser Asn
255      435      440      445
257 Leu Ile Thr Thr Met Glu Asn Thr Lys Phe Gly Gly Val Gly Thr Ser
258      450      455      460
260 Leu Ser Asp Ile Thr Ser Met Ala Glu Gly Glu Leu Ala Ala Lys Leu
261 465      470      475      480
263 Thr Ser Phe Met Phe Gly His Val Val Asn Phe Val Ile Ile Leu Ile
264      485      490      495
266 Val Ile Leu Phe Leu Tyr Cys Met Ile Arg Asn Arg Asn Arg Gln Tyr
267      500      505      510
270 <210> SEQ ID NO: 3

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271 <211> LENGTH: 1464
272 <212> TYPE: DNA
273 <213> ORGANISM: Baculovirus
275 <220> FEATURE:
276 <221> NAME/KEY: CDS
277 <222> LOCATION: (1)..(1464)
280 <400> SEQUENCE: 3
281 atg gta agc gct att gtt tta tat gtg ctt ttg gcg gcg gcg gcg cat      48
282 Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala His
283 1          5          10          15
285 tct gcc ttt gcg gcg gag cac tgc aac gcg caa atg aag acg ggt ccg      96
286 Ser Ala Phe Ala Ala Glu His Cys Asn Ala Gln Met Lys Thr Gly Pro
287          20          25          30
289 tac aag att aaa aac ttg gac att acc ccg ccc aag gaa acg ctg caa      144
290 Tyr Lys Ile Lys Asn Leu Asp Ile Thr Pro Pro Lys Glu Thr Leu Gln
291          35          40          45
293 aag gac gtg gaa atc acc atc gtg gag acg gac tac aac gaa aac gtg      192
294 Lys Asp Val Glu Ile Thr Ile Val Glu Thr Asp Tyr Asn Glu Asn Val
295          50          55          60
297 att atc ggc tac aag ggg tac tac cag gcg tat gcg tac aac ggc ggc      240
298 Ile Ile Gly Tyr Lys Gly Tyr Tyr Gln Ala Tyr Ala Tyr Asn Gly Gly
299 65          70          75          80
301 tcg ctg gat ccc aac aca cgc gtc gaa gaa acc atg aaa acg ctg aat      288
302 Ser Leu Asp Pro Asn Thr Arg Val Glu Glu Thr Met Lys Thr Leu Asn
303          85          90          95
305 gtg ggc aaa gag gat ttg ctt atg tgg agc atc agg cag cag tgc gag      336
306 Val Gly Lys Glu Asp Leu Leu Met Trp Ser Ile Arg Gln Gln Cys Glu
307          100          105          110
309 gtg ggc gaa gag ctg atc gac cgt tgg ggc agt gac agc gac gac tgt      384
310 Val Gly Glu Glu Leu Ile Asp Arg Trp Gly Ser Asp Ser Asp Asp Cys
311          115          120          125
313 ttt cgc gac aac gag ggc cgc ggc cag tgg gtc aaa ggc aaa gag ttg      432
314 Phe Arg Asp Asn Glu Gly Arg Gly Gln Trp Val Lys Gly Lys Glu Leu
315          130          135          140
317 gtg aag cgg cag aat aac aat cac ttt gcg cac cac acg tgc aac aaa      480
318 Val Lys Arg Gln Asn Asn Asn His Phe Ala His His Thr Cys Asn Lys
319 145          150          155          160
321 tcg tgg cga tgc ggc att tcc act tcg aaa atg tac agc agg ctc gag      528
322 Ser Trp Arg Cys Gly Ile Ser Thr Ser Lys Met Tyr Ser Arg Leu Glu
323          165          170          175
325 tgc cag gac gac acg gac gag tgc cag gta tac att ttg gac gct gag      576
326 Cys Gln Asp Asp Thr Asp Glu Cys Gln Val Tyr Ile Leu Asp Ala Glu
327          180          185          190
329 ggc aac ccc atc aac gtg acc gtg gac act gtg ctt cat cga gac ggc      624
330 Gly Asn Pro Ile Asn Val Thr Val Asp Thr Val Leu His Arg Asp Gly
331          195          200          205
333 gtg agt atg att ctc aaa caa aag tct acg ttc acc acg cgc caa ata      672
334 Val Ser Met Ile Leu Lys Gln Lys Ser Thr Phe Thr Thr Arg Gln Ile
335          210          215          220

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/594,690

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Input Set : A:\PTO.RJ.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/594,690

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\10062006\J594690.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date